

In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 4, lines 5-23, and replace it with the following paragraph:

Fig. 1 depict the construction of an oligonucleotide library. FIG. 1(A) The vector fAFF1 contains two non-complementary BstXI sites separated by a 30 bp stuffer fragment (disclosed as SEQ ID NOS 1 and 3, encoding SEQ ID NO: 2). Removal of BstXI fragment (remaining vector fragments disclosed as SEQ ID NOS 4-7, respectively in order of appearance) allows oriented ligation of oligonucleotides with the appropriate cohesive ends ~~(SEQ ID NOS: 1-13)~~ (SEQ ID NO: 131 encoding SEQ ID NOS 9 and 12). Base pairs 1-30 and 49-85 of SEQ ID NO: 131 are disclosed as SEQ ID NOS 8 and 11. Their complements are disclosed as SEQ ID NOS 10 and 13. FIG. 1(B) The oligonucleotide ON-49 was annealed to two "half-site" fragments (SEQ ID NOS 15 and 17) to form cohesive termini complementary to BstXI sites 1 and 2 in the vector. The gapped structure, where the single-stranded region comprises the variable hexacodon sequence and a 2 (gly) codon spacer was ligated to the vector and electro-transformed into E. coli (SEQ ID NO: 130). Base pairs 1-10 and 29-49 of SEQ ID NO: 130 are disclosed as SEQ ID NOS 14 and 16. ~~(SEQ ID NOS:14-17).~~

Please delete the paragraph on page 5, lines 1-3, and replace it with the following paragraph:

FIG. 4 shows the amino acid sequences (deduced from DNA sequence) of the N-terminal peptides of pIII of 52 phage isolated by three rounds of panning on mAB 3E7 (SEQ ID NOS:70-78, 78-91, and 91-119, respectively in order of appearance).

Please delete Table 5 on page 28, and replace it with the following table:

TABLE 5: Relative affinities of peptides for 3E7 antibody determined by solution radioimmunoassay. ^a					
Peptide	<u>SEQ ID NO</u>	N	IC50	(μ M)	Affinity

					Relative to YGGFL <u>(SEQ ID NO: 125)</u>
YGGFL	<u>SEQ ID NO:125</u>	(6)	0.0071	(0.0054,0.0093)	1
YGGF	<u>SEQ ID NO:124</u>	(3)	0.19	(0.093,0.38)	0.037
YGGL	<u>SEQ ID NO:127</u>	(3)	3.8	(2.1,6.6)	0.0018
YGFL	<u>SEQ ID NO:128</u>	(3)	28	(17,47)	0.00025
YGG		(2)	>1000		<0.0000071
GGFL	<u>SEQ ID NO:129</u>	(2)	>1000		<0.0000071
GGF		(2)	>1000		<0.0000071
GFL		(2)	>1000		<0.0000071
YGFWGM	<u>SEQ ID NO:112</u>	(3)	0.35	(0.19,0.63)	0.020
YGPFWs	<u>SEQ ID NO:114</u>	(3)	1.9	(1.3,2.8)	0.0037
YGGFPD	<u>SEQ ID NO:83</u>	(3)	2.3	(1.4,3.7)	0.0031
YGGWAG	<u>SEQ ID NO:79</u>	(3)	7.8	(6.0,10)	0.00091
YGNWTY	<u>SEQ ID NO:104</u>	(3)	7.8	(4.0,15)	0.00091
YAGFAQ	<u>SEQ ID NO:118</u>	(3)	8.3	(3.8,18)	0.00086